

CLUSTAL W (1.82) multiple sequence color alignment

Mus_musculus
Ratus_norvegicus
Oryctolagus_cuniculus
Homo_sapiens
Xenopus_laevis
Aplysia_californica
Drosophila_melanogaster
Caenorhabditis_elegans
Euglena_gracilis
Zea mays

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Ratus_norvegicus
Oryctolagus_cuniculus
Homo_sapiens
Xenopus_laevis
Aplysia_californica
Drosophila_melanogaster
Caenorhabditis_elegans
Euglena_gracilis
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----MLLSVPLLLGLLGLAAADPAIYFKEQFLDGDAWTNRWVESKHKS 44
----MLLSVPLLLGLLGLAAADPAIYFKEQFLDGDAWTNRWVESKHKS 44
-----MLLPVPLLLGLLGLAAAEPVVYFKEQFLDGDGWTERWIESKHKS 44
----MLLSVPLLLGLLGLAVAEPAVYFKEQFLDGDGWTSRWIESKHKS 44
-----LVLPLLA---GLCIAEPAVYFKEEFTDGDGWTQRWVESKHKT 39
-----MKVVLLCALLGIAFADPTVYFKEEF--GDDWAERWVESKHKS 40
----MMWCKTVIVLLATVGFISAEVYLKENF-DNENWEDTWIYSKHPG 43
-----MKSLCLLAIVAVVSAEVYFKEEF-NDASWEKRWVQSKHKD 39
-----MRKELWLGLLLSSQAVLSTIYYKETF--EPDWETRWTHSTAKS 41
MAIRKGSSYAVAALLALASVAAVAGEVFFQEKF--EDGWESRWVKSEWKK 48
                        :: :* + .
---DFGKFVLSSGKFYGDLEKDKGLQTSQDARFYALSAKFEP-FSNKGQT 90
--- DFGKFVLSSGKFYGDQEKDKGLQTSQDARFYALSARFEP-FSNKGQT 90
---DFGKFVLSSGKFYGDQEKDKGLQTSQDARFYALSARFEP-FSNKGQP 90
---DFGKFVLSSGKFYGDEEKDKGLQTSQDARFYALSASFEP-FSNKGQT 90
---DYGKFKLSAGKFYGDSEKDKGLQTSQDARFYAMSSRFDS-FSNKDQT 85
---DLGKFVLTAGKFYGDAEKDKGIQTSQDARFYGLSAKFDK-FSNEGKT 86
K--EFGKFVLTPGTFYNDAEADKGIQTSQDARFYAASRKFDG-FSNEDKP 90
---DFGAFKLSAGKFFDVESRDQGIQTSQDAKFYSRAAKFDKDFSNKGKT 86
---DYGKFKLTSGKFYGDKAKDAGIQTSQDAKFYAISSPIASSFSNEGKD 88
DENMAGEWNHTSGKWNGDAE-DKGIQTSEDYRFYAISAEYPE-FSNKDKT 96
                    * : :.*.: .
LVVQFTVKHEQNIDCGGGYVKLFPSGLDQKDMHGDSEYNIMFGPDICGPG 140
LVVOFTVKHEONIDCGGGYVKLFPGGLDQKDMHGDSEYNIMFGPDICGPG 140
LVVQFTVKHEQNIDCGGGYVKLFPAGLDQKDMHGDSEYNIMFGPDICGPG 140
LVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDICGPG 140
LVVOFSVKHEQNIDCGGGYVKLFPAALEQTEMHEESEYNIMFGPDICGPP 135
LVIQFTVKHEQNIDCGGGYVKVFSSDLDQSDMHGESPYNIMFGPDICGPG 136
LVVQFSVKHEQNIDCGGGYVKLFDCSLDQTDMHGESPYEIMFGPDICGPG 140
LVIQYTVKHEQGIDCGGGYVKVMRADADLGDFHGETPYNVMFGPDICGP- 135
LVLQFSVKHEQDIDCGGGYLKLLPS-VDAAKFTGDTPYHIMFGPDICGA- 136
LVLQFSVKHEQKLDCGGGYVKLLGGDVDQKKFGGDTSYSIMFGPDICGYS 146
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TKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQ 190
TKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQ 190
TKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQ 190
TKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQ 190
TKKVHVIFQYKKKNLQINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSK 185
TKKVHVIFNYKGKNLLVKKDIRCKDDVFSHLYTLIVRPDNTYEVKIDNEK 186
TKKVHVIFSYKGKNHLISKDIRCKDDVYTHFYTLIVRPDNTYEVLIDNEK 190
TRRVHVILNYKGENKLIKKEITCKSDELTHLYTLILNSDNTYEVKIDGES 185
TKKIHFILTYKGKNLLWKKEPRCETDTLSHTYTAVIKADRTYEVLVDQVK 186
TKKVHTILTKDGKNHLIKKDVPCETDQLTHVYTLIIRPDATYSILIDNEE 196
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VESGSLEDDWDFLPPKKIKDPDAAKPEDWDERAKIDDPTDSKPEDWDK-P 239 VESGSLEDDWDFLPPKKIKDPDAAKPEDWDERAKIDDPTDSKPEDWDK-P 239 VESGSLEDDWDFLPPKKIKDPDASKPEDWDERAKIDDPTDSKPEDWDK-P 239 VESGSLEDDWDFLPPKKIKDPDASKPEDWDERAKIDDPTDSKPEDWDK-P 239 VESGSLEDDWDFLPPKKIKDPEAKKPDEWDERPKIDDPEDKKPEDWEK-P 234 AESGDLEADWDFLPAKTIPDPDAKKPDDWDEREKIDDPDDTKPEDWDK-P 235 VESGNLEDDWDFLAPKKIKDPTATKPEDWDDRATIPDPDDKKPEDWDK-P 239 AQTGSLEEDWDLLPAKKIKDPDAKKPEDWDEREYIDDAEDAKPEDWEK-P 234 KESGTLEEDWEILKPKTIPDPEDKKPADWVDEPDMVDPEDKKPEDWDKEP 236 KOTGSIYEHWDILPPKKIKDPEAKKPEDWDDKEYIPDPEDKKPEGYDDIP 246 EHIPDPDAKKPEDWDEEMDGEWEPPVIQNPEYKGEWKPRQIDNPDYKGTW 289 EHIPDPDAKKPEDWDEEMDGEWEPPVIQNPEYKGEWKPRQIDNPDYKGTW 289 EHIPDPDAKKPEDWDEEMDGEWEPPVIQNPEYKGEWKPRQIDNPDYKGTW 289 EHIPDPDAKKPEDWDEEMDGEWEPPVIQNPEYKGEWKPRQIDNPDYKGTW 289 EHIPDPDAVKPEDWDEEMDGEWEPPVIQNPEYKGEWKPRQIDNPDYKGKW 284 EHIPDPEAKKPDDWDDEMDGEWEPPMIDNPEYKGEWKPKQVDNPDYKGKW 285 EHIPDPDATKPEDWDDEMDGEWEPPMIDNPEFKGEWQPKQLDNPNYKGAW 289 EHIPDPDAKKPEDWDDEMDGEWEPPMIDNPEYKGEWKPKQIKNPAYKGKW 284 AQIPDPDATQPDDWDEEEDGKWEAPMISNPKYKGEWKAKKIPNPAYKGVW 286 KEIPDPDAKKPEDWDDEEDGEWTAPTIPNPEYKGPWKQKKIKNPNYQGKW 296 IHPEIDNPEYSPDANIYAYDSFAVLGLDLWQVKSGTIFDNFLITNDEAYA 339 IHPEIDNPEYSPDANIYAYDSFAVLGLDLWQVKSGTIFDNFLITNDEAYA 339 IHPEIDNPEYSPDANIYAYDSFAVLGLDLWQVKSGTIFDNFLITNDEAYA 339 IHPEIDNPEYSPDPSIYAYDNFGVLGLDLWQVKSGTIFDNFLITNDEAYA 339 IHPEIDNPEYTPDDTLYSYDSFGVLGLDLWQVKSGTIFDNFLMTNDEKHA 334 VHPEIDNPEYEADDKLYSFADFGAIGFDLWQVKAGTIFDNVLITDSVEYA 335 EHPEIANPEYVPDDKLYLRKEICTLGFDLWQVKSGTIFDNVLITDDVELA 339 IHPEIENPEYTPDDELYSYESWGAIGFDLWQVKSGTIFDNIIITDSVEEA 334 KPRDIPNPEYEADDKVHIFDEIAAVGFDLWQVKSGTIFDNIIVTDSLAEA 336 KAPMIDNPDFKDDPYIYAFDSLKYIGIELWQVKSGTLFDNIIITDDPALA 346 EEFGNETWGVTKAAEKOMKDKODEEORLKEEEEDKKRKEEEEAE-DKEDD 388 EEFGNETWGVTKAAEKOMKDKODEEORLKEEEEDKKRKEEEEAE-DKEDE 388 EEFGNETWGVTKTAEKQMKDKQDEEQRLKEEEEEEKKRKEEEEAEEDEEDK 389 EEFGNETWGVTKAAEKQMKDKQDEEQRLKEEEEEDKKRKEEEEAE-DKEDD 388 EEYGNETWGVTKEAEKKMKEQQDEEDRKKQEEEEKTRKEEEPQEEEDEDD 384 EEFGNETWGKTKDPEKKMKDAQDEEDRKAREEEEKKRKEEEDANKDDEE- 384 AKAAAEVK-NTQAGEKKMKEAQDEVQRKKDEEEAKKASDKDDEDEDDDD- 387 EAHAAETFDKLKTVEKEKKEKADEETRKAEEEARKKAEEEKEAKKDDDE- 383 KAFYDOTNGATKDAEKKAFDSAEADKRKKEEDERKKQEEEEKKTAEEDE- 385 KTFAEETWGKHKEAEKAAFDEAE--KKKEEEDAAKGGDDEDDDLEDEEDD 394 ... * ** : : * * * * . : : DDR-DEDEDEEDEKEEDEEESPGQAKDEL 416 DDR-DEDEDEEDEKEEDEEDATGQAKDEL 416 DDKEDEDEDEDKDEEEEEAAAGOAKDEL 418 EDKDEDEEDKEEDEEEDVPGQAKDEL 417 DDEEEKEEEKEEEEEEDEEETP--LKDEL 411 ----EEAEEEEEEDDDAAP--EKDEL 405 -----EEKDDESKQDKDQSE---HDEL 406 -----EEKEEEEG-----HDEL 395

EKADEDKADSDAEDSKDSDDEK--QHDEL 421: ***

-----KDEL 401